

RESULT 1
 US-08-323-474-2
 ; Sequence 2, Application US/08323474
 ; Patent No. 5447860
 ; GENERAL INFORMATION:
 ; APPLICANT: Ziegler, Steven F.
 ; TITLE OF INVENTION: NOVEL TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/323,474
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/905,600
 ; FILING DATE: 26-JUN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2609
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-323-474-2

Query Match 100.0%; Score 1708; DB 1; Length 1124;
 Best Local Similarity 100.0%; Pred. No. 3e-155;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALNRKVKNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYA 60
 ||||||||||||||||||
 Db 802 ALNRKVKNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYA 861
 ||||||||||||||||||
 QY 61 SKDDHRDFAGEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRLVLE 120
 ||||||||||||||||||
 Db 862 SKDDHRDFAGEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRLVLE 921
 ||||||||||||||||||
 QY 121 TDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIA 180
 ||||||||||||||||||
 Db 922 TDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIA 981
 ||||||||||||||||||
 QY 181 DFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLWEIVSLGGTPYCG 240
 ||||||||||||||||||
 Db 982 DFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLWEIVSLGGTPYCG 1041
 ||||||||||||||||||
 QY 241 MTCAELYEKLPGQYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKT 300
 ||||||||||||||||||
 Db 1042 MTCAELYEKLPGQYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKT 1101
 ||||||||||||||||||
 QY 301 YVNTTLYEKFTYAGIDCSAEEAA 323
 ||||||||||||||||||
 Db 1102 YVNTTLYEKFTYAGIDCSAEEAA 1124

Sequence Match Listing

RESULT 1

TIE2_HUMAN

ID TIE2_HUMAN STANDARD; PRT: 1124 AA.
AC Q02763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (P140
DE TEK) (Tunica interna endothelial cell kinase) (CD202b antigen).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R.;
RT "Molecular cloning and characterization of a novel receptor protein
RT tyrosine kinase from human placenta.";
RL Oncogene 8:663-670(1993).
RN [2]
RP VARIANT VMCM1 TRP-849.
RX MEDLINE=97134665; PubMed=8980225;
RA Vikkula M., Boon L.M., Cawray K.L. III, Calvert J.T., Diamonti A.J.,
RA Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
RA Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the
RT receptor tyrosine kinase TIE2.";
RL Cell 87:1181-1190(1996).
RN [3]
RP VARIANTS VMCM1 TRP-849 AND SER-897.
RX MEDLINE=99299243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
RA Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasyk K.A.,
RA Speer M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations.";
RL Hum. Mol. Genet. 8:1279-1289(1999).
CC -!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE
CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
CC MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
CC ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
CC PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
CC FORMATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS
CC AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
CC ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
CC -!- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
CC MALFORMATIONS (VMCM1), AN ERROR OF VASCULAR MORPHOGENESIS
CC CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.

CC	-1	SIMILARITY:	BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.	TIE
CC	-1	SUBFAMILY:		
CC	-1	SIMILARITY:	CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.	
CC	-1	SIMILARITY:	CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-1	SIMILARITY:	CONTAINS 3 EGF-LIKE DOMAINS.	
CC	-1	DATABASE:	NAME=PROW; NOTE=PROW 3:12-14(2002); WWW= http://www.ncbi.nlm.nih.gov/prow/guide/1715648914.g.htm "	
CC	-----			
CC	CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	CC	use by non-profit institutions as long as its content is in no way		
CC	CC	modified and this statement is not removed. Usage by and for commercial		
CC	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	CC	or send an email to license@isb-sib.ch) .		
CC	-----			
DR	EMBL:	L06139; AAA61139.1;		
DR	HSSP:	P1362; IFCR.		
DR	Genew:	HGNC:11724; TEK.		
DR	MIM:	600221;		
DR	MIM:	600195;		
DR	InterPro:	IPR000561; EGF-like.		
DR	InterPro:	IPR000719; Euk_pkinase.		
DR	InterPro:	IPR003961; FN_III.		
DR	InterPro:	IPR001245; Tyr_pkinase.		
DR	Pfam:	PF00008; EGF_1.		
DR	Pfam:	PF00041; fn3_3.		
DR	Pfam:	PF00069; pkinase_1.		
DR	PRINTS:	PR00109; TYRKINASE.		
DR	Prodom:	PDO00001; Euk_pkinase; 1.		
DR	SMART:	SM00181; EGF_Z.		
DR	SMART:	SM00001; EGF_Like; 1.		
DR	SMART:	SM00060; FN3_3.		
DR	SMART:	SM00219; TYRKC; 1.		
DR	PROSITE:	PS00107; PROTEIN_KINASE_ADP; 1.		
DR	PROSITE:	PS00109; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE:	PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE:	PS00022; EGF_1; 3.		
DR	PROSITE:	PS01166; EGF_2; 3.		
KM	Receptor:	Tyrosine-protein kinase; Transferrase; Signal; ATP-binding; Repeat: EGF-like domain; Transmembrane; Immunoglobulin domain;		
KW	Glycoprotein:	Phosphorylation; Multigene family; Disease mutation.		
FT	SIGNAL	1	18	POTENTIAL.
FT	CHAIN	19	1124	ANGIOPOIETIN 1 RECEPTOR.
FT	DOMAIN	19	745	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	746	770	POTENTIAL..
FT	DOMAIN	771	1124	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	44	102	IG-LIKE C2-TYPE DOMAIN 1.
FT	DOMAIN	210	252	EGF-LIKE 1.
FT	DOMAIN	254	299	EGF-LIKE 2.
FT	DOMAIN	301	341	EGF-LIKE 3.
FT	DOMAIN	370	424	IG-LIKE C2-TYPE DOMAIN 2.
FT	DOMAIN	444	536	FIBONECTIN TYPE-III 1.
FT	DOMAIN	541	634	FIBONECTIN TYPE-III 2.
FT	DOMAIN	638	732	FIBONECTIN TYPE-III 3.
FT	DOMAIN	824	1096	PROTEIN KINASE.
FT	NP_BIND	830	838	ATP (BY SIMILARITY).
FT	BLINDING	855	855	ATP (BY SIMILARITY).
FT	ACT_SITE	964	964	BY SIMILARITY.
FT	CARBOHYD	140	140	N-LINKED (GLCNAC...)
FT	CARBOHYD	158	158	(POTENTIAL).
FT	CARBOHYD	399	399	N-LINKED (GLCNAC...)
FT	CARBOHYD	438	438	(POTENTIAL).
FT	CARBOHYD	464	464	N-LINKED (GLCNAC...)
FT	CARBOHYD	560	560	(POTENTIAL).
FT	CARBOHYD	596	596	N-LINKED (GLCNAC...)
FT	CARBOHYD	649	649	(POTENTIAL).
FT	CARBOHYD	691	691	N-LINKED (GLCNAC...)
FT	MOD_RES	992	992	(POTENTIAL).
FT	VARIANT	849	849	R -> W (IN VMCM1; ACTIVATING EFFECT).
FT	VARIANT			/FTID-VAR.006352.
FT	VARIANT			Y -> S (IN VMCM1; ACTIVATING EFFECT).
FT	VARIANT			/FTID-VAR.008716.

Seq	SEQUENCE	1124 AA: 125810 MW: 6586050D18FA4CCEC CRF64;
QY	Query Match	100.0%; Score 1708; DB 1; Length 1124;
Db	Best Local Similarity	100.0%; Pred. No. 8e-122;
	Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ALNRKVKNNPPPTIYPLVDMDIKQDYVIGSGNFQVYLKARIKKDGLRMDAIIKRKXEYA 60	
Db	802 ALNRKVKNNPPPTIYPLVDMDIKQDYVIGSGNFQVYLKARIKKDGLRMDAIIKRKXEYA 861	
QY	61 SKDDHRRDAGTELEVYCKIGHHPIINILGAGCHRGYLVLAIEYAPHGNLDFLRKSRVYE 120	
Db	862 SKDDHRRDAGTELEVYCKIGHHPIINILGAGCHRGYLVLAIEYAPHGNLDFLRKSRVYE 921	
QY	121 TDPARAINSTASTLSSOOLHPADVARGMYLSOKPIHRDLAARNILVGENYAKIA 180	
Db	922 TDPARAINSTASTLSSOOLHPADVARGMYLSOKPIHRDLAARNILVGENYAKIA 981	
QY	181 DFGLSGQGVYKTKMGRCLPVRMMATIESLNTSYVTTNSDVSASTGYVLMEIVSLGCTPYCG 240	
Db	982 DFGLSGQGVYKTKMGRCLPVRMMATIESLNTSYVTTNSDVSASTGYVLMEIVSLGCTPYCG 1041	
QY	241 MTCAEVLEKLPQGYRLKPLNCDDVEYDLMROCWRKPYERPFAOILVSLNMLEBKRT 300	
Db	1042 MTCAEVLEKLPQGYRLKPLNCDDVEYDLMROCWRKPYERPFAOILVSLNMLEBKRT 1101	
QY	301 YVNTTYEKETAYAGIDCSAEAA 323	
Db	1102 YVNTTYEKETAYAGIDCSAEAA 1124	